In the Specification:

Please replace paragraph **[21]** beginning at page 5, line 2, with the following:

[21] Figure 1. is a multiple ClustalW DNA Sequence Alignment of sasp-B Amplicons from 38 *Bacillus anthracis* strains (SEQ ID NO:11). Bases 1 - 90 are in Fig. 1A, 91 - 180 are in Fig. 1B, and 181 - 240 are in Fig. 1C.

Please replace paragraph **[22]** beginning at page 5, line 5, with the following:

[22] Figure 2. is a ClustalW multiple sasp-B DNA Sequence Alignment of *Bacillus anthracis*, *Bacillus thuringiensis* and *Bacillus cereus* strains (SEQ ID NOS:12-15, 10, 16, 17-21 and 11, respectively). Bases 1 - 90 are in Fig. 2A, 91 - 180 are in Fig. 2B, and 181 - 240 are in Fig. 2C.

Please replace paragraph **[23]** beginning at page 5, line 9, with the following:

[23] Figure 3. is a representation of *Bacillus globigii* specific PCR primers targeting Bg sasp-gamma (SEQ ID NOS:24 and 25). *B. globigii* sasp-gamma (BgSSPE_edited_) = SEQ ID NO:22; *B. subtilis* sasp-gamma (Bs_pub_SSPE) = SEQ ID NO:23).

Please replace paragraph **[26]** beginning at page 6, line 4, with the following:

[26] Primer sequences were located within each sasp sequence which would maximize the likelihood of amplifying non-homologous sequences. For instance, whenever possible the 3' end of a primer was concluded with one or more thymidine residues. Potential primer sequences were analyzed using Oligo 4.0 primer design software (National Biosciences, Plymouth, MN) for potential hairpin or concatomers,

which might interfere with hybridization to target DNA. Also using Oligo 4.0 primer design software (National Biosciences, Plymouth, MN), primer sequences were adjusted to match their melting temperatures as closely as possible to one another, which generally enhances reaction specificity. The sequence similarity search tool BLAST was queried with the primer sequences in order to insure that the primers did not recognize any bacterial (or other microbial) sequences except the targeted *Bacillus* species. Primers were synthesized (SEQ ID NOS:1-6) (Sequence IDs No.1 through 6) using the PerSeptive Biosystems Expedite nucleic acid synthesis system (Perkin Elmer, Norwalk, Conn.). Oligos were released from columns by incubation in 29.3% ammonium hydroxide at 55°C. overnight, followed by evaporation of ammonium hydroxide using the SpeedVac 1SS110 (Savant Corp.). Primers were resuspended in 10 millimolar tris buffer, pH 8.3, and their concentration measured with a spectrophotometer.

Please replace paragraph **[36]** beginning at page 8, line 29, with the following:

[36] In these alignments, dots signify a match with the sequence shown; only mismatches are spelled out, in order to emphasize them. Primer sequences are not included, but would be extensions of the 5' and 3' ends of the sequences shown.

The *Bacillus anthracis* and *B. cereus* sasp-1 sequence alignment did not show significant differences

```
B.cer     1 CGTAATGAAGTATTAGTTCGAGGCGCTGAACAAGCTCTTGATCAAATGAAATATGAAATT
B.anth    1 .........T............T.....:.....................

B.cer    61 GCACAAGAGTTTGGTGTACAACTTGGTGCAGATACAACAGCTCGTTCAAACGGATCTGTT
B.anth   61 ..................................................T.........

B.cer   121 GGTGGTGAAATTACAAAACGTTTAGTAGCAATGGCAGAACA (SEQ ID NO: 7)
B.anth  121 .................................T..... (SEQ ID NO: 8)
```

The *Bacillus anthracis* and *B. cereus* sasp-2 sequence alignment did not show significant differences

```
B.cer     1 AGCGGTTCCTGGTGCTGAATCAGCATTAGACCAAATGAAATACGAAATCGCTCAAGAGTT
B.anth    1 ............................................................

B.cer    61 TGGTGTTCAACTTGGAGCTGATGCAACAGCTCGCGCTAACGGTTCTGTTGGTGGCGAAAT
B.anth   61 ............................................................

B.cer   121 CACTAAACGTCTAGTTTCACTAGCTGAGCAACAA (SEQ ID NO: 9)
B.anth  121 ............................... (SEQ ID NO: 9)
```

The *Bacillus anthracis* and *B. cereus* sasp-B sequence alignment showed a significant difference, namely a TAGCATT (SEQ ID NO:26) insert

```
BcerPub   1 AACAAAGCAACTTCTGGTGCTAGCATTCAAAGTACAAATGCTAGTTATGGTACAGAGTTT
Banth     1 .....G.......................C.........................

BcerPub  61 TCAACTGAAACAGATGTACAAGCTGTAAAACAAGCAAACGCACAATCAGAAGCAAAGAAA
Banth    61 G.G.........A.........A...........................T......

BcerPub 121 GCACAAGCTTCTGGTGCA------CAAAGTGCAAACGCTAGTTATGGTACAGAATTTGCA
Banth   121 ..G.............TAGCATT.....CA....T.....................

BcerPub 175 ACTGAAACAGACGTGCATTCTGTGAAAAAACAAAATGCTAAGTCAGCTGCAAAACAA
              (SEQ ID NO:10)
Banth   181 .................G.................AC.A.............
              (SEQ ID NO:11)
```

Please replace paragraph **[38]** beginning at page 10, line 9, with the following:

[38] The underlined sequence TAGCATT (SEQ ID NO:26) (SEQ ID NO 107) represents an insertion region useful for distinguishing *Bacillus anthracis* from other *Bacillus* species.

Please replace paragraph **[45]** and TABLE 2. beginning at page 13, line 3, with the following:

[45] Referring now to Figs. 2A, 2B, and 2C, the single *Bacillus anthracis* sequence (#37 which is the bottom row of Figs. 2A, 2B, & 2C) shows a unique pattern of sequence divergence from the sasp-B sequence of these near neighbor isolates. The identities of the sequences are shown in Table 2 below:

TABLE 2.

Legend:

Bacteria	BGSC#	Serotype		Designation
Bacillus licheniformis,		5A2		5A2
Bacillus thuringiensis		4A1	serot-1	4A1
Bacillus thuringiensis		4A3	cry (thur) serot-1	4A3
Bacillus thuringiensis		4J2	aizawai, pacificus/serot-7	4J2
Bacillus thuringiensis	HD3	4B2	2 standard	BtB
Bacillus thuringiensis	HD4	4C3	3a standard	BtC
Bacillus thuringiensis	HD7	4E2	4a4b dendrolimus standard	BtE2
Bacillus thuringiensis		4E4	4a4b	BtE4
Bacillus thuringiensis	HD29	4G5	5a5b	BtG
Bacillus thuringiensis	HD10	4I1	6	BtI
Bacillus thuringiensis	HD11	4J4	7	BtJ
Bacillus thuringiensis	HD12	4K1	8 standard	BtK
Bacillus thuringiensis	HD537 4L3	9 standard		BtL
Bacillus thuringiensis	HD146 4M1	10 standard		BtM
Bacillus thuringiensis	HD201 4N1	11 antisera standard		BtN
Bacillus thuringiensis	HD542 4O1	12 standard		BtO
Bacillus thuringiensis	HD395	4P1	13 standard	BtP
Bacillus thuringiensis	ONR60A	4Q1	14	BtQ
Bacillus thuringiensis	HD511 4R1	15		BtR
Bacillus thuringiensis	HD521 4S2	16 standard		BtS
Bacillus thuringiensis	HD525 4T1	no flagellar antigen		BtT
Bacillus thuringiensis	HD541 4U1	11a11c		BtU
Bacillus thuringiensis		4V1	17	BtV
Bacillus thuringiensis	HD 867	4W1	18	BtW
Bacillus thuringiensis	IS720	4X1	21	BtX
Bacillus thuringiensis	HD868	4Y1	19 standard	BtY
Bacillus thuringiensis	HD501	4Z1	8a8c standard	BtZ
Bacillus anthracis	BA42D	11		NMRI#11

Unidentified *Bacillus*			003
Unidentified *Bacillus*		Taken from filled bag in "final mixing trailer"	1B
Unidentified *Bacillus*		Isolated from 1B culture as morphologically distinct colonies	1B/A
Unidentified *Bacillus*		Isolated from 25kg media drum, bentonite mixture	III
Unidentified *Bacillus*		Isolated from bentonite spore stock	IV
Bacillus cereus	Genbank #M16813	NCBI Genbank database	Bcerpub
Bacillus cereus	ATCC 14579	Purchased from ATCC	Bcer1
Bacillus cereus	ATCC 11778	Purchased from ATCC	Bcer2
Bacillus cereus	ATCC 6464	Purchased from ATCC	Bcer3

BGSC is the Bacillus Genetic Stock Center, at The Ohio State University.

Please replace paragraph **[46]** and TABLE 3. beginning at page 15, line 4, with the following:

[46] Based on the DNA sequence information in Figures 1 and 2, amino acid sequences were extrapolated and evaluated for the sasp-B genes from *Bacillus anthracis*, *Bacillus cereus* and *Bacillus thuringiensis*. These extrapolated sequences are shown below in an extrapolated amino acid sequence alignments for the sasp-B gene from *Bacillus anthracis*, *Bacillus cereus* and *Bacillus thuringiensis*. The identities of the sequences are shown in Table 3.

```
          1               15 16              30 31              45 46              60
1 4D4     NKATSGASIQSTNAS YGTEFSTETDVQAVK QANAQSEAKKAQASG A--QSANASYGTEFA
2 Bcerp   NKATSGASIQSTNAS YGTEFSTETDVQAVK QANAQSEAKKAQASG A--QSANASYGTEFA
3 BtK     NKATSGASIQSTNAS YGTEFATETNVQAVK QANAQSEAKKAQASG A--QSANASYGTEFA
4 BtB     NKATSGASIQSTNAS YGTEFSTETDVQAVK QANAQSEAKKAQASG A--QSANASYGTEFA
5 Banth   NKATSGASIQSTNAS YGTEFATETNVQAVK QANAQSEAKKAQASG ASIQSTNASYGTEFA
6 Bmyc    NKATSGASIQSTNAS YGTEFATETNVQAVK QANAQSEAQKAQASA A--QSANASYGTEFA

          61              75 76
1 4D4     TETDVHSVKKQNAKS AAKQ (SEQ ID NO:27)
2 Bcerp   TETDVHSVKKQNAKS AAKQ (SEQ ID NO:27)
3 BtK     TETDVHAVKKQNAKS AAKQ (SEQ ID NO:28)
4 BtB     TETDVHAVKKQNAQS AAKQ (SEQ ID NO:29)
5 Banth   TETDVHAVKKQNAQS AAKQ (SEQ ID NO:30)
6 Bmyc    TETDVHAVKKQNAQS AAK  (SEQ ID NO:31)
```

TABLE 3.

Legend:

Bacteria	BGSC#	Serotype	Designation
Bacillus thuringiensis	type strain		4D4
Bacillus thuringiensis	HD12	4K1 8 standard	BtK
Bacillus thuringiensis	HD3	4B2 2 standard	BtB
Bacillus cereus published sequence		GenBank #M16813	Bcerp
Bacillus mycoides		ATCC 6421, subtype Flugge	Bmyc
Bacillus anthracis			Banth

Please replace paragraph **[47]** beginning at page 16, line 7, with the following:

[47] In the previous examples, the BcSasp-B primers were useful for evaluating the prevalence of the unique *Bacillus anthracis* sasp-B signature, but sequencing was required to distinguish amplicons of the several *Bacillus* species which could be amplified using the *Bacillus cereus* primers. By studying the alignment of *Bacillus anthracis* and *Bacillus cereus* sasp-B sequences (above) potential anthracis specific primer and probe sites were identified (shown below, SEQ ID NOS:32 and 33). Eight oligonucleotides were designed with the aid of Oligo 4.0 and BLAST database search utilities then synthesized (all as described in Example 1 above) and evaluated

experimentally in various combinations for their ability to prime amplification of *Bacillus anthracis* only, using a panel of near neighbor *Bacillus* species. Three of the primer pairs were designed to incorporate the *Bacillus anthracis* insertion region into the three prime end of one primer per pair. This strategy greatly limited amplicon size and did not leave any *Bacillus anthracis* specific sequence for probe design.

Please replace paragraph **[48]** beginning at page 16, line 19, with the following:

[48] The combination of primers originally designated BaSPB7 and BaSPB8 (below) were sufficiently specific. From 100 nanograms *B. cereus* target a very faint product band of nearly (but not exactly) the correct size, was evident; when compared to signals from an amplified dilution series of *Bacillus anthracis* DNA, the signal from *Bacillus cereus* was approximately equivalent to product from 10 picograms - indicating 10,000 fold less efficient amplification. Bands were not visible at or near the correct size from products of *Bacillus coagulans*, *Bacillus circulans*, *Bacillus globigii*, *Bacillus mycoides*, *Bacillus subtilis* or *Bacillus thuringiensis* amplification.

Please replace paragraph **[49]** beginning at page 16, line 27, with the following:

[49] In addition, these primers were for sequences flanking, rather than incorporating the *Bacillus anthracis* insertion region, thus leaving this region within the product for binding to probes designed to hybridize to this unique signature.

The *Bacillus anthracis* primer data (from analysis by Oligoprimer design software, National Biosciences, Plymouth, MN.) is summarized as follows:

BaSPB7 primer sequence:

5' GTT ATG GTA CAG AGT TTG CG 3' (SEQ ID NO:32)

Tm = 57.4 °C (salt 1000.0 mM; oligo 0.6 pM)

Td = 57.6 °C, G(25°C) = -34.7 kcal/mol, Mr = 6283

Ext. coeff.: 5.05 nmol/A260, 31.7 µg/A260

BaSPB8 primer sequence:

5' TTG TTT TGC AGC TGA TTG T 3' (SEQ ID NO:33)

Tm = 58.3 °C (salt 1000.0 mM; oligo 0.6 pM)

Td = 58.9 °C, G(25°C) = -34.1 kcal/mol, Mr = 5911

Ext. coeff.: 5.82 nmol/A260, 34.4 µg/A260

Please replace paragraph **[51]** beginning at page 17, line 20, with the following:

[51] Thermalcycling: Amplifications were performed in a Perkin Elmer 9600 thermocycler with the following thermal cycling regime: 94°C for 5 minutes, then 40 repeating cycles of 94°C for 30 seconds, 50°C for 30 seconds and 72°C for 30 seconds, followed by a 7 minute 72°C final extension step.

Please replace paragraph **[52]** beginning at page 17, line 24, with the following:

[52] Reaction mixture: Each 100ul reaction contained 0.1 millimolar each dATP, dCTP, dGTP and dTTP, 25 picomoles each primer, 10 millimolar Tris-HCl pH 8.3, 2 millimolar $MgCl_2$, 25 millimolar KCl, 2.5 units of Taq polymerase (Perkin Elmers, Norwalk, Conn.) and 100 ng or less of template DNA.

The uniqueness of these primers may be seen by a *Bacillus anthracis* and *Bacillus cereus* sasp-B sequence alignment emphasizing *Bacillus anthracis* specific primer sequences:

```
BcerPub    1 AACAAAGCAACTTCTGGTGCTAGCATTCAAAGTACAAATGCTAGTTATGGTACAGAGTTT
Banth      1 .....G.........................C.........GTTATGGTACAGAGTTT
                                                      --primer BaSPB7--

BcerPub   61 TCAACTGAAACAGATGTACAAGCTGTAAAACAAGCAAACGCACAATCAGAAGCAAAGAAA
Banth     61 GCG.........A.........A............................T......
              --> (SEQ ID NO:32)

BcerPub  121 GCACAAGCTTCTGGTGCA------CAAAGTGCAAACGCTAGTTATGGTACAGAATTTGCA
Banth    121 ..G.............TAGCATT.....CA....T.....................

BcerPub  175 ACTGAAACAGACGTGCATTCTGTGAAAAAACAAAATGCTAAGTCAGCTGCAAAACAAA
(SEQ ID NO:10)
Banth    181 ...:.............G..................ACAATCAGCTGCAAAACAAA
(SEQ ID NO:11)
                                        (SEQ ID NO:33) <--primer BaSPB8---
```

Please replace paragraph **[53]** beginning at page 18, line 15, with the following:

[53] The *Bacillus anthracis* and *Bacillus cereus* sasp-B sequence alignment shows the sequence similarity between the present *Bacillus anthracis* sasp B DNA (which is a 240 base pair amplicon as described above) and the corresponding region of its most similar known sequence, the *Bacillus cereus* sasp B gene. This alignment, run in the CLUSTALW program described herein, yields a similarity score of 89%, using default parameters. As is known in the art, the default parameters for nucleic acid pairwise alignments are gap opening penalty = 15; gap extension penalty = 6.66. The IUB matching protocol is used -All matches score 1.9; all mismatches for IUB symbols

score 0. The CLUSTAL matching protocol can also be used. In this case, matches score 1.0 and mismatches score 0.0. In either case, CLUSTALW comparison of the *Bacillus anthracis* sasp B DNA and the comparable *Bacillus cereus* sasp B DNA yields a score of 89%.--

Please replace paragraph **[55]** beginning at page 18, line 31, with the following:

--**[55]** In the present case, a BLAST search revealed that the closest sequence corresponds to the *Bacillus cereus* small acid-soluble spore protein, Accession Number M16813. This corresponds with the discussion in this Example. Using BLAST parameters, the two nucleotide sequences have an identity of 86%.--

Please replace paragraph **[57]** beginning at page 19, line 6, with the following:

--**[57]** Accordingly, those of skill in the art would recognize that the Sasp-B DNA of *Bacillus anthracis* is homologous but not identical to that of *Bacillus cereus*. Thus, this invention includes any sasp-B from *Bacillus anthracis* that might include minor single base differences (polymorphisms) from SEQ ID NO:11, yet, maintain the insert of SEQ ID NO:26.

Please replace paragraph **[58]** beginning at page 19, line 14, with the following:

--**[58]** Three of the oligonucleotides evaluated as primers incorporated the *Bacillus anthracis* specific insertion region, and having designed primers flanking the insertion region, these oligos were tested as probes to confirm the identity of the amplicons; only amplicons from *B. anthracis* would include the 6 base insertion, as follows:

Alignment of *Bacillus cereus* and *Bacillus anthracis* Sasp-B sequences emphasizing probed locations

```
Bcer   AACAAAGCAACTTCTGGTGCTAGCATTCAAAGTACAAATGC
Banth  AACAAGGCAACTTCTGGTGCTAGCATTCAAAGCACAAATGC

Bcer   TAGTTATGGTACAGAGTTTTCAACTGAAACAGATGTACAAGCTGTAAAACAAGCAAACGCACAA
Banth  TAGTTATGGTACAGAGTTTGCGACTGAAACAAATGTACAAGCAGTAAAACAAGCAAACGCACAA

Bcer   TCAGAAGCAAAGAAAGCACAAGCTTCTGGTGCA------CAAAGTGCAAACGCTAGTTATGGTACAGAATTTGCAA
Banth  TCAGAAGCTAAGAAAGCGCAAGCTTCTGGTGCTAGCATTCAAAGCACAAATGCTTTGCATAGTTATGGTACAGAAA
                                  ---------------------- BaSPB4
                                  ---------------------- BaSPB2
                          ↑    location of probes tested   ↑

Bcer   CTGAAACAGACGTGCATTCTGTGAAAAAACAAAATGCTAAGTCAGCTGCAAAACAA (SEQ ID NO:10)
Banth  CTGAAACAGACGTGCATGCTGTGAAAAAACAAAATGCACAATCAGCTGCAAAACAA (SEQ ID NO:11)
```

Three oligonucleotides evaluated for use as *Bacillus anthracis* probes:

BaSPB2: (inverted, 'lower strand' sequence): 5' GCATTTGTGCTTTGAATGCTA 3' (SEQ ID NO:34)
BaSPB4: (inverted, 'lower strand' sequence): 5' CATTTGTGCTTTGAATGCTA 3' (SEQ ID NO:35)
BaSPB5: (direct, 'upper strand' sequence): 5' AGCTTCTGGTGCTAGCATT 3' (SEQ ID NO:36)--

Please replace paragraph **[63]** beginning at page 20, line 34, with the following:

--**[63]** Finally, probe BaSPB4 was tested for specificity. Fifty nanograms of DNA from each of the following *Bacillus* species was amplified using biotinylated BaSPB7 and BaSPB8: *Bacillus anthracis*, *Bacillus thuringiensis*, *Bacillus cereus*, *Bacillus mycoides*, *Bacillus subtilis*, and *Bacillus globigii*. The denatured amplicon of each DNA species was reacted against the bound BaSPB4 probe and the test strips developed. Only the *Bacillus anthracis* amplicon resulted in any signal (which was quite intense); none of the other species bound to the probe in order to result in a signal. Conclusion: BaSPB4 binds *Bacillus anthracis* DNA specifically. BaSPB4 binding

specificity was demonstrated with the BioRad universal GeneComb System (data not shown). 100 ng of each species of DNA amplified was placed on each panel, as follows (1 - 8):

Species Amplified:

1) *Bacillus anthracis*

2) *Bacillus thuringiensis*

3) *Bacillus cereus*

4) *Bacillus mycoides*

5) *Bacillus subtilis*

6) *Bacillus globigii*

7) Negative PCR

8) Kit positive control--

Please replace paragraph **[71]** beginning at page 22, line 16, with the following:

--**[71]** In the same manner as described in Example 1 above, a sasp gene (sasp-gamma in this case) sequence was identified for the production of primers specific for *Bacillus globigii* sequence. Primers and amplification conditions were designed (see Figure 3) for heterologous PCR based on published sequence for the *Bacillus subtilis* sasp E gene (sasp-gamma) acquired from GenBank (accession number M16184). After sequencing amplicons from *Bacillus globigii* (generated using the *Bacillus subtilis* primers), and aligning *Bacillus globigii* sequence with the published *Bacillus subtilis* sequence, *Bacillus globigii* specific primers were designed taking advantage of the differences in the sequence. After searching the databases to be sure that the new *Bacillus globigii* primers were not homologous to other sequences, and optimizing amplification conditions, a panel of *Bacillus* species were amplified to check primer specificity. Amplicons of the correct size were produced only from *Bacillus* designated as *Bacillus globigii*, for all but the most arcane intents and purposes (there is

disagreement among a very few researchers as to whether *Bacillus subtilis niger* and *Bacillus atrophaeus* are, in fact, genetically different from *Bacillus globigii* at all); importantly, the new primers did not amplify *Bacillus subtilis* or *Bacillus amyloliquifaciens* - which are distinct species, yet very closely related to *Bacillus globigii*. Referring now to Fig. 3, there is shown an alignment of *Bacillus subtilis* sasp-gamma sequence (from Genbank) (Bs_pub_SSPE) with *Bacillus globigii* sequence (upper strand) showing the location of the primer sequences and how their sequence compares to the known *Bacillus subtilis* sequence.--

Please replace paragraph **[72]** beginning at page 23, line 3, with the following:

--**[72]** The BgSaspGam primers produce *Bacillus globigii* specific PCR product, as was demonstrated in an Nuseive-Agarose gel (data not shown). The gel showed approximately a 135b *Bacillus globigii* specific amplicon. No amplification of negative controls in *Bacillus cereus*; *Bacillus amyoliquifaciens*, *Bacillus megaterium*, or *Bacillus globisporus* was observed. Amplification was observed with *Bacillus atropheus* (ATCC 6455 and 49337) and *Bacillus subtilis niger*. It should be noted that *Bacillus subtilis niger* and *Bacillus atrophaeus* have been officially designated *Bacillus globigii* since they are virtually indistinguishable from *Bacillus globigii* at the molecular level. Near neighbors *Bacillus subtilis*, *Bacillus globisporus* and *Bacillus megatarium* do not amplify with the BgSaspGam primers.

Bacillus globigii sasp-gamma primers:

BgSaspGam 5'	5' ACATGGCTAACTCAAACAACAA 3' (SEQ ID NO:24)
BgSaspGam 3'	5' GGTTTTGTTTTCTTACTTGTTGTAC 3' (SEQ ID NO:25)--

Please replace paragraph **[77]** beginning at page 24, line 2, with the following:

--**[77]** In a manner similar to the above descriptions, a sasp gene (sasp-2 in this case) sequence was identified for the production of primers for amplification of *Clostridium perfringens* sequence. Primers and amplification conditions were designed and carried out using *Clostridium perfringens* DNA. While amplification successfully produced product of the correct size (when viewed by ethidium bromide gel electrophoresis), near neighbor DNA has yet to be evaluated in order to assess specificity of these primers.

Clostridium perfringens sasp-2 primers:

CPssp2-1: 5' AATAACTAAGGAGGAATGAAAAATGT 3' (SEQ ID NO:37)

Cpssp2-2: 5' TTGTTCTACCATTCTTTTAACCATT 3' (SEQ ID NO:38)--

Please replace paragraph **[83]** beginning at page 24, line 35, with the following:

--**[83]** Having described the present invention, it will be apparent that other embodiments are possible in light of the present teachings. For example, other DNA amplification methods besides PCR are known, such as the Q-beta replicase method. Certain of these methods may be used in a single-step amplification/detection protocol, based, for example, on the unique *Bacillus anthracis* sasp-B insertion TAGCATT (SEQ ID NO:26) (SEQ ID NO 107).--

Please replace paragraph **[85]** beginning at page 25, line 10, with the following:

--**[85]** The novel sasp polypeptides of the invention can also be used to produce antibodies which are specifically immunoreactive or bind to epitopes of the sasp polypeptides. Antibodies of the invention specifically include antibodies which bind to